

## SEQUENCE LISTING

<110> Istituto Superiore di Sanità  
National Institutes of Health

<120> COLORECTAL ANTIGEN

<130> WPP88367

<150> US 60/512,040

<151> 2003-10-15

<160> 20

<170> PatentIn version 3.3

<210> 1

<211> 1413

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (85)..(1395)

<220>

<221> misc\_feature

<222> (1180)..(1240)

<223> nucleotide sequence encoding the immunogenic peptide

<400> 1

```

cgctgcggga cggctagcgg ccctgcgtgg aggcgaggaa tccgcatcta tggagatgtc      60
cctgcatccc atgactcgga gctg atg gcc ttc atg acg agg aag ttg tgg      111
                Met Ala Phe Met Thr Arg Lys Leu Trp
                1                      5

gac ctg gag cag cag gtg aag gcc cag act gat gag ata ctg tcc aag      159
Asp Leu Glu Gln Gln Val Lys Ala Gln Thr Asp Glu Ile Leu Ser Lys
10                      15                      20                      25

gat cag aag ata gcg gcc cta gag gac ctg gtg cag acc ctc cgg cca      207
Asp Gln Lys Ile Ala Ala Leu Glu Asp Leu Val Gln Thr Leu Arg Pro
30                      35                      40

cac cca gcc gag gca acc ctg cag cgg cag gag gaa ctg gag acg atg      255
His Pro Ala Glu Ala Thr Leu Gln Arg Gln Glu Glu Leu Glu Thr Met
45                      50                      55

tgt gtg cag ctg cag cgg cag gtc agg gag atg gag cgg ttc ctc agt      303
Cys Val Gln Leu Gln Arg Gln Val Arg Glu Met Glu Arg Phe Leu Ser
60                      65                      70

gac tat ggc ctg cag tgg gtg ggc gag ccc atg gac cag gag gac tca      351
Asp Tyr Gly Leu Gln Trp Val Gly Glu Pro Met Asp Gln Glu Asp Ser
75                      80                      85

gag agc aag aca gtc tca gag cat ggc gag agg gac tgg atg aca gcc      399
Glu Ser Lys Thr Val Ser Glu His Gly Glu Arg Asp Trp Met Thr Ala
90                      95                      100                      105

aag aag ttc tgg aag cca ggg gac tca ttg gcg ccc cct gag gtg gac      447
Lys Lys Phe Trp Lys Pro Gly Asp Ser Leu Ala Pro Pro Glu Val Asp
110                      115                      120

ttt gac agg ctg ctg gcc agc ctg cag gat ctt agt gag ctg gtg gta      495
Phe Asp Arg Leu Leu Ala Ser Leu Gln Asp Leu Ser Glu Leu Val Val

```

125	130	135	
gag ggt gac acc caa gtg aca cca gtg ccc ggc ggg gca cgg ctg cgt Glu Gly Asp Thr Gln Val Thr Pro Val Pro Gly Gly Ala Arg Leu Arg 140 145 150			543
acc ctc gag ccc atc ccg ctg aag ctc tac cgg aat ggc atc atg atg Thr Leu Glu Pro Ile Pro Leu Lys Leu Tyr Arg Asn Gly Ile Met Met 155 160 165			591
ttc gac ggg ccc ttc cag ccc ttc tac gat ccc tcc aca cag cgc tgc Phe Asp Gly Pro Phe Gln Pro Phe Tyr Asp Pro Ser Thr Gln Arg Cys 170 175 180 185			639
ctc cga gac ata ttg gat ggc ttc ttt ccc tca gag ctc cag cga ctg Leu Arg Asp Ile Leu Asp Gly Phe Phe Pro Ser Glu Leu Gln Arg Leu 190 195 200			687
tac ccc aat ggg gtc ccc ttt aag gtg agt gac ttg cgc aat cag gtc Tyr Pro Asn Gly Val Pro Phe Lys Val Ser Asp Leu Arg Asn Gln Val 205 210 215			735
tac ctg gag gat gga ctg gac ccc ttc cca ggc gag ggc cgt gtg gtg Tyr Leu Glu Asp Gly Leu Asp Pro Phe Pro Gly Glu Gly Arg Val Val 220 225 230			783
ggc agg cag cgg atg cac aag gcc ttg gac agg gtg gag gag cac cca Gly Arg Gln Arg Met His Lys Ala Leu Asp Arg Val Glu Glu His Pro 235 240 245			831
ggc tcc agg atg act gct gag aaa ttt ctg aac agg ctc ccc aag ttt Gly Ser Arg Met Thr Ala Glu Lys Phe Leu Asn Arg Leu Pro Lys Phe 250 255 260 265			879
gtg atc cgg caa ggc gag gtg att gac atc cgg ggc ccc atc agg gac Val Ile Arg Gln Gly Glu Val Ile Asp Ile Arg Gly Pro Ile Arg Asp 270 275 280			927
acc ttg cag aac tgc tgc cca ttg cct gcc cgg atc cag gag att gtg Thr Leu Gln Asn Cys Cys Pro Leu Pro Ala Arg Ile Gln Glu Ile Val 285 290 295			975
gtg gag acg ccc acc ttg gcc gct gag cga gag agg agc cag gag tca Val Glu Thr Pro Thr Leu Ala Ala Glu Arg Glu Arg Ser Gln Glu Ser 300 305 310			1023
ccc aac aca ccg gca ccc ccg ctc tcc atg ctg cgc atc aag tct gag Pro Asn Thr Pro Ala Pro Pro Leu Ser Met Leu Arg Ile Lys Ser Glu 315 320 325			1071
aat ggg gaa cag gcc ttc cta ctg atg atg cag cct gac aac acc att Asn Gly Glu Gln Ala Phe Leu Leu Met Met Gln Pro Asp Asn Thr Ile 330 335 340 345			1119
ggg gac gtg cga gct ctg cta gcg cag gcc agg gtc atg gat gcc tct Gly Asp Val Arg Ala Leu Leu Ala Gln Ala Arg Val Met Asp Ala Ser 350 355 360			1167
gcc ttt gag atc ttc agc aca ttc ccg ccc acc ctc tac cag gac gat Ala Phe Glu Ile Phe Ser Thr Phe Pro Pro Thr Leu Tyr Gln Asp Asp 365 370 375			1215
aca ctc acg ctg cag gct gca ggc ctt gtg ccc aaa gca gca ctg ctg Thr Leu Thr Leu Gln Ala Ala Gly Leu Val Pro Lys Ala Ala Leu Leu 380 385 390			1263
ctg cgg gca cgc cga gcc ccg aag tcc agc ctg aaa ttc agt cct ggt Leu Arg Ala Arg Arg Ala Pro Lys Ser Ser Leu Lys Phe Ser Pro Gly			1311

395                      400                      405  
 ccc tgt ccc ggt ccc ggt ccc ggc ccc agt ccc ggt ccc ggt ccc ggc      1359  
 Pro Cys Pro Gly Pro Gly Pro Gly Pro Ser Pro Gly Pro Gly Pro Gly  
 410                      415                      420                      425  
  
 tcc agt ccc tgt ccc gga ccc agt ccc agc ccc caa taaagcaccc      1405  
 Ser Ser Pro Cys Pro Gly Pro Ser Pro Ser Pro Gln  
                          430                      435  
  
 accccctc      1413  
  
 <210> 2  
 <211> 437  
 <212> PRT  
 <213> Homo sapiens  
  
 <400> 2  
 Met Ala Phe Met Thr Arg Lys Leu Trp Asp Leu Glu Gln Gln Val Lys  
 1                      5                      10                      15  
  
 Ala Gln Thr Asp Glu Ile Leu Ser Lys Asp Gln Lys Ile Ala Ala Leu  
                          20                      25                      30  
  
 Glu Asp Leu Val Gln Thr Leu Arg Pro His Pro Ala Glu Ala Thr Leu  
                          35                      40                      45  
  
 Gln Arg Gln Glu Glu Leu Glu Thr Met Cys Val Gln Leu Gln Arg Gln  
                          50                      55                      60  
  
 Val Arg Glu Met Glu Arg Phe Leu Ser Asp Tyr Gly Leu Gln Trp Val  
 65                      70                      75                      80  
  
 Gly Glu Pro Met Asp Gln Glu Asp Ser Glu Ser Lys Thr Val Ser Glu  
                          85                      90                      95  
  
 His Gly Glu Arg Asp Trp Met Thr Ala Lys Lys Phe Trp Lys Pro Gly  
                          100                      105                      110  
  
 Asp Ser Leu Ala Pro Pro Glu Val Asp Phe Asp Arg Leu Leu Ala Ser  
                          115                      120                      125  
  
 Leu Gln Asp Leu Ser Glu Leu Val Val Glu Gly Asp Thr Gln Val Thr  
                          130                      135                      140  
  
 Pro Val Pro Gly Gly Ala Arg Leu Arg Thr Leu Glu Pro Ile Pro Leu  
 145                      150                      155                      160  
  
 Lys Leu Tyr Arg Asn Gly Ile Met Met Phe Asp Gly Pro Phe Gln Pro  
                          165                      170                      175  
  
 Phe Tyr Asp Pro Ser Thr Gln Arg Cys Leu Arg Asp Ile Leu Asp Gly  
                          180                      185                      190

Phe Phe Pro Ser Glu Leu Gln Arg Leu Tyr Pro Asn Gly Val Pro Phe  
 195 200 205  
 Lys Val Ser Asp Leu Arg Asn Gln Val Tyr Leu Glu Asp Gly Leu Asp  
 210 215 220  
 Pro Phe Pro Gly Glu Gly Arg Val Val Gly Arg Gln Arg Met His Lys  
 225 230 235 240  
 Ala Leu Asp Arg Val Glu Glu His Pro Gly Ser Arg Met Thr Ala Glu  
 245 250 255  
 Lys Phe Leu Asn Arg Leu Pro Lys Phe Val Ile Arg Gln Gly Glu Val  
 260 265 270  
 Ile Asp Ile Arg Gly Pro Ile Arg Asp Thr Leu Gln Asn Cys Cys Pro  
 275 280 285  
 Leu Pro Ala Arg Ile Gln Glu Ile Val Val Glu Thr Pro Thr Leu Ala  
 290 295 300  
 Ala Glu Arg Glu Arg Ser Gln Glu Ser Pro Asn Thr Pro Ala Pro Pro  
 305 310 315 320  
 Leu Ser Met Leu Arg Ile Lys Ser Glu Asn Gly Glu Gln Ala Phe Leu  
 325 330 335  
 Leu Met Met Gln Pro Asp Asn Thr Ile Gly Asp Val Arg Ala Leu Leu  
 340 345 350  
 Ala Gln Ala Arg Val Met Asp Ala Ser Ala Phe Glu Ile Phe Ser Thr  
 355 360 365  
 Phe Pro Pro Thr Leu Tyr Gln Asp Asp Thr Leu Thr Leu Gln Ala Ala  
 370 375 380  
 Gly Leu Val Pro Lys Ala Ala Leu Leu Leu Arg Ala Arg Arg Ala Pro  
 385 390 395 400  
 Lys Ser Ser Leu Lys Phe Ser Pro Gly Pro Cys Pro Gly Pro Gly Pro  
 405 410 415  
 Gly Pro Ser Pro Gly Pro Gly Pro Gly Ser Ser Pro Cys Pro Gly Pro  
 420 425 430  
 Ser Pro Ser Pro Gln  
 435

<210> 3  
 <211> 60  
 <212> DNA  
 <213> Homo sapiens

<400> 3  
 ttcagcacat tcccgccac cctctaccag gacgatacac tcacgctgca ggctgcaggc 60

<210> 4  
 <211> 20  
 <212> PRT  
 <213> Homo sapiens

<400> 4

Phe Ser Thr Phe Pro Pro Thr Leu Tyr Gln Asp Asp Thr Leu Thr Leu  
 1 5 10 15

Gln Ala Ala Gly  
 20

<210> 5  
 <211> 42  
 <212> DNA  
 <213> Homo sapiens

<400> 5  
 accctctacc aggacgatac actcacgctg caggctgcag gc 42

<210> 6  
 <211> 14  
 <212> PRT  
 <213> Homo sapiens

<400> 6

Thr Leu Tyr Gln Asp Asp Thr Leu Thr Leu Gln Ala Ala Gly  
 1 5 10

<210> 7  
 <211> 1028  
 <212> DNA  
 <213> Homo sapiens

<400> 7  
 ctcaagtact atggcctgca gtgggtgggc gagcccatgg accaggagga ctcaagagagc 60  
 aagacagtct cagagcatgg cgagagggac tggatgacag ccaagaagtt ctggaagcca 120  
 ggggactcat tggcgcccc tgaggtggac tttgacaggc tgctggccag cctgcaggat 180  
 cttagtgagc tgggtggtaga gggtagacac caagtgacac cagtgcccg cggggcacgg 240  
 ctgcgtaccc tcgagcccat cccgctgaag ctctaccgga atggcatcat gatgttcgac 300  
 gggcccttcc agcccttcta cgatccctcc acacagcgct gcctccgaga catattggat 360  
 ggcttctttc cctcagagct ccagcgactg taccccaatg ggggtcccctt taaggtgagt 420  
 gacttgcgca atcaggtcta cctggaggat ggactggacc ccttcccagg cgagggccgt 480  
 gtgggtgggca ggcagcggat gcacaaggcc ttggacaggg tggaggagca cccaggctcc 540  
 aggatgactg ctgagaaatt tctgaacagg ctccccaagt tttgatccgg caaggcgagg 600  
 tgattgacat ccggggcccc atcagggaca ccttgagaa ctgctgcccc ttgcctgccc 660

ggatccagga gattgtggtg gagacgcca ccttgccgc tgagcgagag aggagccagg 720  
 agtcacccaa cacaccggca ccccgctct ccatgctgcg catcaagtct gagaatggg 780  
 aacaggcctt cctactgatg atgcagcctg acaacaccat tggggacgtg cgagctctgc 840  
 tagcgcaggc cagggctatg gatgcctctg cctttgagat cttcagcaca ttcccgcca 900  
 ccctctacca ggacgataca ctcacgctgc aggctgcagg ccttgtgccc aaagcagcac 960  
 tgctgctgcg ggcacgccga gccccgaagt ccagcctgaa attcagtcct ggtccctgtc 1020  
 ccggtccc 1028

<210> 8  
 <211> 343  
 <212> PRT  
 <213> Homo sapiens

<400> 8

Leu Ser Asp Tyr Gly Leu Gln Trp Val Gly Glu Pro Met Asp Gln Glu  
 1 5 10 15

Asp Ser Glu Ser Lys Thr Val Ser Glu His Gly Glu Arg Asp Trp Met  
 20 25 30

Thr Ala Lys Lys Phe Trp Lys Pro Gly Asp Ser Leu Ala Pro Pro Glu  
 35 40 45

Val Asp Phe Asp Arg Leu Leu Ala Ser Leu Gln Asp Leu Ser Glu Leu  
 50 55 60

Val Val Glu Gly Asp Thr Gln Val Thr Pro Val Pro Gly Gly Ala Arg  
 65 70 75 80

Leu Arg Thr Leu Glu Pro Ile Pro Leu Lys Leu Tyr Arg Asn Gly Ile  
 85 90 95

Met Met Phe Asp Gly Pro Phe Gln Pro Phe Tyr Asp Pro Ser Thr Gln  
 100 105 110

Arg Cys Leu Arg Asp Ile Leu Asp Gly Phe Phe Pro Ser Glu Leu Gln  
 115 120 125

Arg Leu Tyr Pro Asn Gly Val Pro Phe Lys Val Ser Asp Leu Arg Asn  
 130 135 140

Gln Val Tyr Leu Glu Asp Gly Leu Asp Pro Phe Pro Gly Glu Gly Arg  
 145 150 155 160

Val Val Gly Arg Gln Arg Met His Lys Ala Leu Asp Arg Val Glu Glu  
 165 170 175

His Pro Gly Ser Arg Met Thr Ala Glu Lys Phe Leu Asn Arg Leu Pro  
 180 185 190

Lys Phe Val Ile Arg Gln Gly Glu Val Ile Asp Ile Arg Gly Pro Ile  
 195 200 205

Arg Asp Thr Leu Gln Asn Cys Cys Pro Leu Pro Ala Arg Ile Gln Glu  
 210 215 220

Ile Val Val Glu Thr Pro Thr Leu Ala Ala Glu Arg Glu Arg Ser Gln  
 225 230 235 240

Glu Ser Pro Asn Thr Pro Ala Pro Pro Leu Ser Met Leu Arg Ile Lys  
 245 250 255

Ser Glu Asn Gly Glu Gln Ala Phe Leu Leu Met Met Gln Pro Asp Asn  
 260 265 270

Thr Ile Gly Asp Val Arg Ala Leu Leu Ala Gln Ala Arg Val Met Asp  
 275 280 285

Ala Ser Ala Phe Glu Ile Phe Ser Thr Phe Pro Pro Thr Leu Tyr Gln  
 290 295 300

Asp Asp Thr Leu Thr Leu Gln Ala Ala Gly Leu Val Pro Lys Ala Ala  
 305 310 315 320

Leu Leu Leu Arg Ala Arg Arg Ala Pro Lys Ser Ser Leu Lys Phe Ser  
 325 330 335

Pro Gly Pro Cys Pro Gly Pro  
 340

<210> 9  
 <211> 6  
 <212> PRT  
 <213> Homo sapiens

<400> 9

Phe Ser Thr Phe Pro Pro  
 1 5

<210> 10  
 <211> 6  
 <212> PRT  
 <213> Homo sapiens

<400> 10

Leu Val Pro Lys Ala Ala  
 1 5

<210> 11  
 <211> 294  
 <212> DNA  
 <213> Homo sapiens

<400> 11  
 ggggacgtgc gagctctgct agcgaggcc agggatcatgg atgcctctgc ctttgagatc 60  
 ttcagcacat tcccgccac cctctaccag gacgatacac tcacgtgca ggctgcaggc 120  
 cttgtgcca aagcagcact gctgctgagg gcacggcag cccgaagtc cagcctgaaa 180  
 ttcagtctg gtccctgtcc cgggtccggg cccggcccca gtcccggtcc cgggtccggg 240  
 tccagtcct gtcccgacc cagtccagc cccaataaaa gcacccacc cctc 294

<210> 12  
 <211> 92  
 <212> PRT  
 <213> Homo sapiens

<400> 12

Gly Asp Val Arg Ala Leu Leu Ala Gln Ala Arg Val Met Asp Ala Ser  
 1 5 10 15

Ala Phe Glu Ile Phe Ser Thr Phe Pro Pro Thr Leu Tyr Gln Asp Asp  
 20 25 30

Thr Leu Thr Leu Gln Ala Ala Gly Leu Val Pro Lys Ala Ala Leu Leu  
 35 40 45

Leu Arg Ala Arg Arg Ala Pro Lys Ser Ser Leu Lys Phe Ser Pro Gly  
 50 55 60

Pro Cys Pro Gly Pro Gly Pro Gly Pro Ser Pro Gly Pro Gly Pro Gly  
 65 70 75 80

Ser Ser Pro Cys Pro Gly Pro Ser Pro Ser Pro Gln  
 85 90

<210> 13  
 <211> 19  
 <212> DNA  
 <213> ARTIFICIAL

<220>  
 <223> PCR primer sequence

<400> 13  
 tccagcatgg tgtgtctga 19

<210> 14  
 <211> 18  
 <212> DNA  
 <213> artificial

<220>  
 <223> PCR primer sequence

<400> 14  
 ccttgaatgt ggtcatct 18



<210> 15  
 <211> 23  
 <212> DNA  
 <213> artificial

<220>  
 <223> PCR primer sequence

<400> 15  
 cgtttcttgg agtactctac gtc 23

<210> 16  
 <211> 20  
 <212> DNA  
 <213> artificial

<220>  
 <223> PCR primer sequence

<400> 16  
 ccaccgcggc ccgctcgtct 20

<210> 17  
 <211> 20  
 <212> PRT  
 <213> Homo sapiens

<400> 17

Phe Ser Thr Phe Pro Pro Thr Leu Tyr Gln Asp Asp Thr Leu Thr Leu  
 1 5 10 15

Gln Ala Ala Gly  
 20

<210> 18  
 <211> 20  
 <212> PRT  
 <213> Homo sapiens

<400> 18

Thr Leu Tyr Gln Asp Asp Thr Leu Thr Leu Gln Ala Ala Gly Leu Val  
 1 5 10 15

Pro Lys Ala Ala  
 20

<210> 19  
 <211> 1771  
 <212> DNA  
 <213> Homo sapiens

<400> 19  
 aaaaaaccgc gtgacaacaa gatggcggcg ctgcgggacg gctagcggcc ctgcgtgtac 60  
 ttccccaagc accaccaggc caaaggtctc tcagttcaga gcagaaagcc gtatacccag 120  
 aggagcaggc agataacaga aacttcaga aacctctgtg gagacagtgg aagaggcaaa 180  
 agggagtcc tgacagctgg attctagaag tagaactatg agctcacctt tggcctccct 240

tagcaagacc cgaaaagtgc ccctgccctc ggagcctatg aatcctggga ggcgaggaat 300  
 ccgcatctat ggagatgaag atgaggtgga catgttgagt gatgggtgtg gctcggaaga 360  
 aaagatctca gtcccttcct gctatggcgg cataggtgcc cctgtgagtc ggcaagtccc 420  
 tgcaccccat gactcggagc tgatggcctt catgacgagg aagttgtggg acctggagca 480  
 gcaggtgaag gccagactg atgagatact gtccaaggat cagaagatag cggccctaga 540  
 ggacctggtg cagaccctcc ggccacaccc agccgaggca accctgcagc ggcaggagga 600  
 actggagacg atgtgtgtgc agctgcagcg gcaggtcagg gagatggagc ggttcctcag 660  
 tgactatggc ctgcagtggg tgggcgagcc catggaccag gaggactcag agagcaagac 720  
 agtctcagag catggcgaga gggactggat gacagccaag aagttctgga agccagggga 780  
 ctcatggcg cccctgagg tggactttga caggctgctg gccagcctgc aggatcttag 840  
 tgagctggtg gtagagggtg acaccaagt gacaccagt cccggcgggg cacggctgcg 900  
 taccctcgag cccatcccg cgaagctcta ccggaatggc atcatgatgt tcgacggggc 960  
 cttccagccc ttctacgac cctccacaca gcgctgcctc cgagacatat tggatggctt 1020  
 ctttcctca gagctccagc gactgtacc caatggggtc cctttaagg tgagtgactt 1080  
 gcgcaatcag gtctacctg aggatggact ggacccctc ccaggcgagg gccgtgtggt 1140  
 gggcaggcag cggatgcaca aggccttgga cagggtggag gagcaccag gctccaggat 1200  
 gactgctgag aaatttctga acaggctccc caagtttgtg atccggcaag gcgaggtgat 1260  
 tgacatccgg ggccccatca gggacacctt gcagaactgc tgccattgc ctgccggat 1320  
 ccaggagatt gtggtggaga cggcacctt ggccgctgag cgagagagga gccaggagtc 1380  
 acccaacaca ccggcacccc cgctctccat gctgcgcac aagtctgaga atggggaaca 1440  
 ggcttccta ctgatgatgc agcctgacaa caccattggg gacgtgcgag ctctgctagc 1500  
 gcaggccagg gtcattgatg cctctgcctt tgagatcttc agcacattcc cggccacct 1560  
 ctaccaggac gataactca cgctgcaggc tgcaggcctt gtgcccagg cagcactgct 1620  
 gctgcgggca cggcgagccc cgaagtccag cctgaaattc agtctgtgtc cctgtcccgg 1680  
 tcccggtccc ggccccagtc ccgggtcccg tcccggtccc agtccctgtc ccggaccag 1740  
 tccagcccc caataaagca cccgccccct c 1771

&lt;210&gt; 20

&lt;211&gt; 512

&lt;212&gt; PRT

&lt;213&gt; Homo sapiens

&lt;400&gt; 20

Met Ser Ser Pro Leu Ala Ser Leu Ser Lys Thr Arg Lys Val Pro Leu  
 1 5 10 15

Pro Ser Glu Pro Met Asn Pro Gly Arg Arg Gly Ile Arg Ile Tyr Gly  
 20 25 30

Asp Glu Asp Glu Val Asp Met Leu Ser Asp Gly Cys Gly Ser Glu Glu  
 35 40 45  
 Lys Ile Ser Val Pro Ser Cys Tyr Gly Gly Ile Gly Ala Pro Val Ser  
 50 55 60  
 Arg Gln Val Pro Ala Ser His Asp Ser Glu Leu Met Ala Phe Met Thr  
 65 70 75 80  
 Arg Lys Leu Trp Asp Leu Glu Gln Gln Val Lys Ala Gln Thr Asp Glu  
 85 90 95  
 Ile Leu Ser Lys Asp Gln Lys Ile Ala Ala Leu Glu Asp Leu Val Gln  
 100 105 110  
 Thr Leu Arg Pro His Pro Ala Glu Ala Thr Leu Gln Arg Gln Glu Glu  
 115 120 125  
 Leu Glu Thr Met Cys Val Gln Leu Gln Arg Gln Val Arg Glu Met Glu  
 130 135 140  
 Arg Phe Leu Ser Asp Tyr Gly Leu Gln Trp Val Gly Glu Pro Met Asp  
 145 150 155 160  
 Gln Glu Asp Ser Glu Ser Lys Thr Val Ser Glu His Gly Glu Arg Asp  
 165 170 175  
 Trp Met Thr Ala Lys Lys Phe Trp Lys Pro Gly Asp Ser Leu Ala Pro  
 180 185 190  
 Pro Glu Val Asp Phe Asp Arg Leu Leu Ala Ser Leu Gln Asp Leu Ser  
 195 200 205  
 Glu Leu Val Val Glu Gly Asp Thr Gln Val Thr Pro Val Pro Gly Gly  
 210 215 220  
 Ala Arg Leu Arg Thr Leu Glu Pro Ile Pro Leu Lys Leu Tyr Arg Asn  
 225 230 235 240  
 Gly Ile Met Met Phe Asp Gly Pro Phe Gln Pro Phe Tyr Asp Pro Ser  
 245 250 255  
 Thr Gln Arg Cys Leu Arg Asp Ile Leu Asp Gly Phe Phe Pro Ser Glu  
 260 265 270  
 Leu Gln Arg Leu Tyr Pro Asn Gly Val Pro Phe Lys Val Ser Asp Leu  
 275 280 285  
 Arg Asn Gln Val Tyr Leu Glu Asp Gly Leu Asp Pro Phe Pro Gly Glu  
 290 295 300

Gly Arg Val Val Gly Arg Gln Arg Met His Lys Ala Leu Asp Arg Val  
305 310 315 320

Glu Glu His Pro Gly Ser Arg Met Thr Ala Glu Lys Phe Leu Asn Arg  
325 330 335

Leu Pro Lys Phe Val Ile Arg Gln Gly Glu Val Ile Asp Ile Arg Gly  
340 345 350

Pro Ile Arg Asp Thr Leu Gln Asn Cys Cys Pro Leu Pro Ala Arg Ile  
355 360 365

Gln Glu Ile Val Val Glu Thr Pro Thr Leu Ala Ala Glu Arg Glu Arg  
370 375 380

Ser Gln Glu Ser Pro Asn Thr Pro Ala Pro Pro Leu Ser Met Leu Arg  
385 390 395 400

Ile Lys Ser Glu Asn Gly Glu Gln Ala Phe Leu Leu Met Met Gln Pro  
405 410 415

Asp Asn Thr Ile Gly Asp Val Arg Ala Leu Leu Ala Gln Ala Arg Val  
420 425 430

Met Asp Ala Ser Ala Phe Glu Ile Phe Ser Thr Phe Pro Pro Thr Leu  
435 440 445

Tyr Gln Asp Asp Thr Leu Thr Leu Gln Ala Ala Gly Leu Val Pro Lys  
450 455 460

Ala Ala Leu Leu Leu Arg Ala Arg Arg Ala Pro Lys Ser Ser Leu Lys  
465 470 475 480

Phe Ser Pro Gly Pro Cys Pro Gly Pro Gly Pro Gly Pro Ser Pro Gly  
485 490 495

Pro Gly Pro Gly Ser Ser Pro Cys Pro Gly Pro Ser Pro Ser Pro Gln  
500 505 510